

ATGAGAAGGTGTAGAATAAGTGGGAGGCCCCCGGCGCCCCCGGTGTCCCCGCCAGGCC
MetArgArgCysArgIleSerGlyArgProProAlaProProGlyValProAlaGlnAla

CCTGTCTCCCAGCCTGATGCCCCCTGGCCACCAGAGGAAAGTGGTGTTCATGGATAGATGTG
ProValSerGlnProAspAlaProGlyHisGlnArgLysValValSerTrpIleAspVal

TATACTCGCGCTACCTGCCAGCCCCGGGAGGTGGTGGTGGCCCTTGACTGTGGAGCTCATG
TyrThrArgAlaThrCysGlnProArgGluValValValProLeuThrValGluLeuMet

GGCACCGTGGCCAAACAGCTGGTGGCCAGCTGCGTGAAGTGTGCAGCGCTGTGGTGGCTGC
GlyThrValAlaLysGlnLeuValProSerCysValThrValGlnArgCysGlyGlyCys

TGCCCTGACGATGGCCTGGAGTGTGTGCCCCACTGGGCAGCACCAAGTCCGGATGCAGATC
CysProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMetGlnIle

CTCATGATCCGGTACCCGAGCAGTCAGCTGGGGGAGATGTCCCTGGAAGAACACAGCCAG
LeuMetIleArgTyrProSerSerGlnLeuGlyGluMetSerLeuGluGluHisSerGln

TGTGAATGCAGACCTAAAAAAAAGGACAGTGCTGTGAAGCCAGACAGGGCTGCTACTCCC
CysGluCysArgProLysLysLysAspSerAlaValLysProAspArgAlaAlaThrPro

CACCACCGTCCCCAGCCCCGTTCTGTTCCGGGCTGGGACTCTGCCCCCGGAGCACCTCC
HisHisArgProGlnProArgSerValProGlyTrpAspSerAlaProGlyAlaProSer

CCAGCTGACATCACCCAATCCCACTCCAGCCCCAGGCCCTCTGCCCACGCTGCACCCAG
ProAlaAspIleThrGlnSerHisSerSerProArgProLeuCysProArgCysThrGln

CACCACCAGTGCCCTGACCCCCGACCTGCCGCTGCCGCTGTCGACGCCGAGCTTCCTC
HisHisGlnCysProAspProArgThrCysArgCysArgCysArgArgArgSerPheLeu

CGTTGTCAAGGGCGGGGCTTAGAGCTCAACCCAGACACCTGCAGGTGCCGGAAGCTGCGA
ArgCysGlnGlyArgGlyLeuGluLeuAsnProAspThrCysArgCysArgLysLeuArg

AGGTGA
ArgEnd

FIGURE 1

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      10      20      30      40      50
MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNH-EVVKFMDVYQSYC
      ::||::: ::::|: :||::||| |: |
MRRCRISGRPPAPPGVPAQAPVSQPDAPGHQKVVSWIDVYTRATC

      60      70      80      90     100     110
HPIETLVDIFQEYPDEIEYIFKPSCVPLMRGGCCNDEGLECVPTESNITMQIMRIKPH
:| |::| : | :::: : |||:: ||||| |:|||||||:: :: ||::|: :
QPREVVVPLTVELMGTVAKQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIR-Y

      120     130           140     150     160
QQQHIGEMSFLQHNKCECRPKK-----DRA-----RQEKKSVRGKGKGQKRKRKKSRY
:: ::|||: :|::||| ||| |:: :||:| :::: : :
PSSQLGEMSLEEHSQCECRPKKDSAVKPDRAATPHHRPQPRSVPGWDSAPGAPSPADIT

      170     180     190     200     210
KSWSVPCGPCSERRKHLFVQDPQTCKCCKNTD-SRCKARQLELNERTCRCDKPRR
:| | | : | :||:|:|:|: : ||::| ||| ||| | ||
QSHSSPRPLCPRCTQHHQCPDPRTCRCRCRRRSFLRCQGRGLELNPDTCRCRKLRR

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Figure 2. Sequence alignment of VEGF3(lower line) compared to VEGF from human (upper line).

FIGURE 2 1/1